

AMENDMENTS TO THE SPECIFICATION:

Please replace the original title with the following title:

"POLYNUCLEOTIDES ENCODING hOCTN1 POLYPEPTIDE"

Please replace the paragraph beginning at page 17, line 5 with the following paragraph:

Fig. 3 compares the sequence of human OCTN1 (SEQ ID NO:1) with human OCTN2 (SEQ ID NO:3). Amino acid residues conserved in both transporters are shaded. Sequences coinciding with the consensus sequences of sugar transporter and the ATP/GTP binding site are indicated by "+" and "*", respectively.

Please replace the paragraph beginning at page 10, line 13 with the following paragraph:

It is routine for those skilled in the art to obtain proteins functionally equivalent to the transporter proteins of this invention by isolating and using DNAs highly homologous to the DNA sequences encoding the transporter proteins of this invention (human OCTN1, human OCTN2, mouse OCTN1, and mouse OCTN2) or portions thereof using hybridization techniques (Sambrook, J. et al., Molecular Cloning 2nd ed., 9.47-9.58, Cold Spring Harbor Lab. press, 1989), etc. These proteins functionally equivalent to those of transporter proteins of this invention are also included in proteins of this invention. Here, "functionally equivalent" means that proteins have an activity to transport organic cations. DNAs that hybridize to the DNAs encoding the proteins of this invention can be isolated from other organisms, for example, rats, rabbits, cattle, etc. as well as humans and mice. Especially, tissues such as the kidney are suitable as sources of such DNAs. These DNAs isolated using hybridization techniques usually have a high homology with the above-described DNAs encoding the transporter proteins of this invention. "High homology" means at least 70% or more, preferably at least 80% or more, and more preferably at least 90% or more of amino acid sequence identity. The "percent identity" of two amino acid sequences or of two nucleic acids is determined using the algorithm of Karlin and Altschul (Proc. Natl. Acad. Sci. USA 87:2264-2268, 1990), modified as in Karlin and Altschul (Proc. Natl. Acad. Sci. USA 90:5873-5877, 1993). Such an algorithm is incorporated into the NBLAST and XBLAST programs of Altschul et al. (J. Mol. Biol. 215:403-410, 1990). BLAST nucleotide searches

are performed with the NBLAST program, score=100, wordlength=12. BLAST protein searches are performed with the XBLAST program, score=50, wordlength=3. Where gaps exist between two sequences, Gapped BLAST is utilized as described in Altschul et al. (Nucleic Acids Res. 25:3389-3402, 1997). When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) are used. See <http://www.ncbi.nlm.nih.gov>.